

87163

From: Slobodyansky, Elizabeth
Sent: Friday, February 21, 2003 11:28 PM
To: STIC-Biotech/ChemLib
Subject: 09/590,375

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FEB 24 2003

Please align SEQ ID NO:1 in the above application with SEQ ID NO: 4 in US 6,197,565.

Thank you.

Elizabeth Slobodyansky, PhD

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Searcher: _____
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TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Slobodansky
04/15/98 375
USC1975C5

> 0 <
01 10 Intelligenetics
> 0 <

GENALIGN Multiple Sequence Alignment Program
Release 5.4

Mon 24 Feb 103 10:49:49-PSY

Solution Parameters:

Amino Alphabet - Identity
Output line length - 80
Compress - Off
Histogram - Off
Randomization - Off
AMINO-Res-length - 2
Deletion-weight - 5.00
Length-factor - 0
Matching-weight - 1.00
NUCLEIC-Res-length - 4
Spread-factor - 50

Clustered order of selected sequences:

4. US-09-193-468-4 (1-483)
9. US-09-590-375-1 (1-480)

Region Alignment: (listed in clustered order)

```
09-193- 1 aNLNGTlMOYfEMyMNDGQHWRLndpsAYlaengITAWtIPPAKGS:SOADVGYAYDL
-590- 1 dGLNGTmmOYEmhLndGQHWRLndbaALsdagITAlMIPPAKGS:SOADVGYAYDL
consensus --LNCT-MOY-EW---NDGQHW-RL--D-A-L---GITA-WIPPAKGS-SOADVGYAYDL

US-09-193- 62 YDLGEFHOKGTVRTYGTGtqelqSAIKSLHSFDINVGDDVlnHKgGADATEDVCAveYp
US-09-590- 62 YDLGEFHOKGTVRTYGTGtqelqSAIKSLHSFDINVGDDVlnHKgGADATEDVCAveYp
consensus YDLGEF-QKGTVRTYGTG--L-AI-SL-S-DINVGDDV--NHK-GAD-TE-V-AV-V-P

US-09-193- 123 adRatVISGehliKAmThPhPGKgsCYSDfKwMyhNEdGLWDdesrklnrIyKfgqkwd
US-09-590- 123 tnrWqdiSGaYLiDAmTgfdFagRnnaySDfKwrfHfngGVMDqgrYgenhi ffrAntm
consensus --R---ISG---I-AWT--F-F-GR---YSDFKW-W-HF-G-DWD-----N-I--F-----W-

US-09-193- 184 WeVnENGNYDYlMyadIDydhPVAaeIKrWGLyaneELqLdGfRLDAVKHikPsflJrdW
US-09-590- 184 WtVdEENGNYDYlLgnsnIDfshPevqdeIKGGSWfcdELdDgyRLDAIKHlPfwYtsDW
consensus W-V--ENGNYDYL-----ID--HP-V--E-K-WG-W---EL-LDG-RLDA-KHI-F-----DW

US-09-193- 245 VnHvReKtGkemfVAEYwqndIGALEnYlnKtfnhsVFDVPLhyqfhaastOGGgYDMR
US-09-590- 245 VtHqRneadqdlFvYgveYwkdVgALefYldemNwemsIFDVPLInfyfyrASQGSYDMR
consensus V-H-R-----F-V-EYW--D-GALE-YL---N--S-FDVPL-Y-F--AS-QGG-YDMR

US-09-193- 306 kLlNGctvyskHPlkavTFVNDNHDPGGSLSestYgtwFKPLAYAlFILRREGSpqVfyGDM
US-09-590- 306 nLlRGSlyeahPhmhaVTfVDNDHDPGGSLSesWadwFKPLAYAlILTRREGgYpNvfyGdy
consensus --L-G-V-V-HP---VTFVDNHDPGGSLSes-V--WFKPLAYA-ILTRR-GYP-VfyGD-
```

```
US-09-193- 367 YGtKgsqreIPAlKKhlePILKARKqYAYGaOHDFDHDlVGWTRREGSSVANSGLAl
US-09-590- 367 YG 1pndnIsakkdmIdelldARqnYAYGtOHDFDHDVdVVGWTRREGSSStPNSGLAl
consensus YGtKg-----I-A-K--I---L-AR---YAYG-OHDYFDH-D-VGWTREG-SS--NSGLA--
```

```
US-09-193- 428 ItdGPGaKtMYGRONAGetWHDlTGNrsepyvInseGGEFhVNGGSVlYqr
US-09-590- 425 msnGPGsKwMYGRONAGtWCDlTGmngasYlIngdGGEFfLNGGSVSYVnq
consensus ---GPGG-K-MYGRONAG-TW-D-TGN-----V-IN--GWGEF--NGGSVS-YV--
```

Alignment score = 286.00

Scoring matrix:

4	4
9	9
281	

